

REMARKS/ARGUMENTS

I. Status of the claims

Claims 1, 18, 21, 22, 34, 43, 60 and 61 are amended with entry of this amendment. Claims 1-7, 9-23, 25-35, 37-38, and 40-61 are pending with entry of this Amendment.

The amendments merely re-arrange the wording of the claims and therefore do not add new matter.

II. Claim Objections

Claims 21 and 22 were objected to as allegedly unclear. The Examiner requested that the word "selected" be added to further clarify the claims. Although Applicants assert that the claims are clear as drafted, to expedite prosecution, the word is inserted by this Amendment.

III. Rejection under 35 U.S.C. § 112, second paragraph

Claims 1-7, 9-23, 25-35, 37, 38, and 40-61 were rejected as allegedly indefinite. Applicants respectfully traverse the rejection.

With regard to claim 1, the Examiner indicated that the third step was unclear. Specifically, she asked whether the "for which there are 5 or fewer..." limitation was intended to limit the primers or the repeat-free subsequences. Although Applicants submit that the claims are clear as drafted, the language objected to by the Examiner has been re-written to further clarify the claims:

As amended, the third step of claim 1 reads as follows:
executing a third process on a digital computer to identify, based on the repeat sequence-free subsequences, oligonucleotide sequences that are suitable for use as primers in an amplification reaction to amplify a product within at least one of said repeat sequence-free subsequences, wherein the nucleotide sequence database contains 5 or fewer sequences at least 50% identical to the repeat-free subsequence from which the oligonucleotide sequence is identified

Claims 1-42 generally include three steps: 1) removing repeat sequences, 2) comparing the remaining repeat-free subsequences to a database to identify sequences, if any, in the database at least 50% identical to the repeat-free subsequences, and 3) generating primers to amplify a repeat-free subsequence that has 5 or fewer sequences at least 50% identical to it in the database. The limitation also limits the *pool* of repeat-free subsequences from which the primer sequences may be selected. By limiting which repeat-free subsequences are available, step three is ultimately a limitation on the possible primers. Thus, the claims provide a limitation in the third step which was not described in the art.

Note that claims 43-61 are somewhat different. Those claims include the steps of: 1) removing repeat sequences, 2) comparing the remaining repeat-free subsequences to a database to identify sequences, if any, in the database at least 50% identical to the repeat-free subsequences, and discarding at least one repeat-free subsequence with at least 50% identity, and 3) generating primers to amplify a repeat-free subsequence that remains after the at least one repeat-free subsequence with at least 50% identity is discarded. In these claims, the third step involves selecting primer sequences from a pool of sequences that is smaller than merely a pool of repeat-free subsequences compared to a database. Specifically, the pool is depleted for repeat-free subsequences that have significant (50%) identity with sequences in the database.

Thus, in all of the independent claims, the step of "selecting oligonucleotides for use as primers" provides a limitation by allowing only for selection of primers that either do not have a certain percent identity (as in claims 1-42) or that are selected from a pool of repeat-free subsequences that are depleted of sequences with family members in the database (claims 43-61). Both sets of claims thereby select for primer sequences that would only amplify unique sequences in the genome, thereby identifying, e.g. single copy probes useful for FISH experiments.

Finally, the Examiner questioned whether the oligonucleotides were intended to be selected "based upon the identified regions." To clarify, the phrase "based on the repeat sequence-free subsequences" was inserted into the claims. Thus, although Applicants believe the

Appl. No. 09/766,450
Amdt. dated June 1, 2004
Amendment under 37 CFR 1.116 Expedited Procedure
Examining Group

PATENT

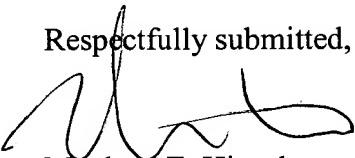
claims were clear before, as amended the claims expressly indicate that the oligonucleotide sequences are generated from the repeat sequence-free subsequences.

In view of the above explanation, Applicants respectfully request that the Examiner withdraw the remaining rejections.

CONCLUSION

In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance and an action to that end is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,

Matthew E. Hinsch
Reg. No. 47,651

TOWNSEND and TOWNSEND and CREW LLP
Two Embarcadero Center, Eighth Floor
San Francisco, California 94111-3834
Tel: 415-576-0200
Fax: 415-576-0300
Attachments
MEH:meh
60227299 v1